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NEWS 7 DEC 27 CA/CAplus enhanced with more pre-1907 records
NEWS 8 JAN 08 CHEMLIST enhanced with New Zealand Inventory of Chemicals
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NEWS 10 JAN 16 IPC version 2007.01 thesaurus available on STN
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multiple databases
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NEWS 19 FEB 26 MEDLINE reloaded with enhancements
NEWS 20 FEB 26 EMBASE enhanced with Clinical Trial Number field
NEWS 21 FEB 26 TOXCENTER enhanced with reloaded MEDLINE
NEWS 22 FEB 26 IFICDB/IFIPAT/IFIUDB reloaded with enhancements
NEWS 23 FEB 26 CAS Registry Number crossover limit increased from 10,000

to 300,000 in multiple databases
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NEWS 25 MAR 16 CASREACT coverage extended
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NEWS 28 MAR 30 RDISCLOSURE reloaded with enhancements
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NEWS 30 APR 02 JICST-EPLUS removed from database clusters and STN

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=> s (chymotrypsin or trypsin or elastase or cathepsin or granzyme or
chymase or tryptase) (4A) (domain or fragment or subunit or region or
epitope or motif)
L1        6054 (CHYMOTRYPSIN OR TRYPSIN OR ELASTASE OR CATHEPSIN OR
GRANZYME
               OR CHYMASE OR TRYPTASE) (4A) (DOMAIN OR FRAGMENT OR
SUBUNIT OR
              REGION OR EPITOPE OR MOTIF)

=> s (two hybrid)
L2       39797 (TWO HYBRID)

=> s l1 and l2
L3          11 L1 AND L2

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L4             5 DUPLICATE REMOVE L3 (6 DUPLICATES REMOVED)

=> d l4 1-5 bib ab

L4   ANSWER 1 OF 5  CAPLUS  COPYRIGHT 2007 ACS on STN
AN   2004:218251  CAPLUS
DN   140:370674
TI   The SANT2 Domain of the Murine Tumor Cell DnaJ-like Protein 1
Human
     Homologue Interacts with α1-Antichymotrypsin and Kinetically
     Interferes with Its Serpin Inhibitory Activity
AU   Kroczynska, Barbara; Evangelista, Christina M.; Samant, Shalaka
S.;
     Elguindi, Ebrahim C.; Blond, Sylvie Y.
CS   Department of Medicinal Chemistry and Pharmacognosy, College of
Pharmacy,
     Center for Pharmaceutical Biotechnology, University of Illinois,
Chicago,
     IL, 60607-7173, USA
SO   Journal of Biological Chemistry (2004), 279(12), 11432-11443.
     CODEN: JBCHA3; ISSN: 0021-9258
PB   American Society for Biochemistry and Molecular Biology
DT   Journal
LA   English
AB   The murine tumor cell DnaJ-like protein 1 or MTJ1/ERdj1 is a
membrane
     J-domain protein enriched in microsomal and nuclear fractions.
We
     previously showed that its lumenal J-domain stimulates the
ATPase activity
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of the mol. chaperone BiP/GRP78 (Chevalier, M., Rhee, H., Elguindi, E. C., and Blond, S. Y. (2000) J. Biol. Chemical 275, 19620-19627). MTJ1/ERdj1 also contains a large carboxyl-terminal cytosolic extension composed of two tryptophan-mediated repeats or SANT domains for which the function(s) is unknown. Here we describe the cloning of the human homolog HTJ1 and its interaction with α1-antichymotrypsin (ACT), a member of the serine proteinase inhibitor (serpin) family. The interaction was initially identified in a two-hybrid screening and further confirmed in vitro by dot blots, native electrophoresis, and fluorescence studies. The second SANT domain of HTJ1 (SANT2) was found to be sufficient for binding to ACT, both in yeast and in vitro. Single tryptophan-alanine substitutions at two strictly conserved residues significantly (Trp-497) or totally (Trp-520) abolished the interaction with ACT. SANT2 binds to human ACT with an intrinsic affinity equal to 0.5 nM. Preincubation of ACT with nearly stoichiometric concns. of SANT2 wild-type but not SANT2:W520A results in an apparent loss of ACT inhibitory activity toward chymotrypsin. Kinetic anal. indicates that the formation of the covalent inhibitory complex ACT-chymotrypsin is significantly delayed in the presence of SANT2 with no change on the catalytic efficiency of the enzyme. This work demonstrates for the first time that the SANT2 domain of MTJ1/HTJ1/ERdj1 mediates stable and high affinity protein-protein interactions.

RE.CNT 72 THERE ARE 72 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 2 OF 5 CAPLUS COPYRIGHT 2007 ACS on STN
AN 2003:656314 CAPLUS
DN 139:194002
TI Combinatorial libraries of protein monomer domains and their use in developing proteins with novel binding and interaction properties
IN Kolkman, Joost A.; Stemmer, Willem P. C.; Govindarajan, Sridhar
PA USA
SO U.S. Pat. Appl. Publ., 118 pp., Cont.-in-part of U.S. Ser. No. 133,128.

CODEN: USXXCO
DT Patent
LA English
FAN.CNT 11

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI US 2003157561	A1	20030821	US 2002-289660	20021106
WO 2002088171	A2	20021107	WO 2002-US13257	20020426
WO 2002088171	A3	20030508		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZM, ZW				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
US 2003082630	A1	20030501	US 2002-133128	20020426
US 2004175756	A1	20040909	US 2003-693057	20031024
US 2005048512	A1	20050303	US 2003-693056	20031024
CA 2504670	A1	20040527	CA 2003-2504670	20031106
WO 2004044011	A2	20040527	WO 2003-US35664	20031106
WO 2004044011	A3	20060420		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM,				

TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW
RW: BW, GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ,
BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE,
ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK,
TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

AU	2003295426	A1	20040603	AU 2003-295426 20031106
EP	1587843	A2	20051026	EP 2003-786612 20031106
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, HU, SK			
US	2005053973	A1	20050310	US 2004-840723 20040505
US	2005089932	A1	20050428	US 2004-871602 20040617
US	2006223114	A1	20061005	US 2005-281245 20051116
US	2006286603	A1	20061221	US 2006-392108 20060328
PRAI US	2001-337209P	P	20011119	
US	2001-333359P	P	20011126	
US	2002-374107P	P	20020418	
US	2002-133128	A2	20020426	
WO	2002-US13257	A	20020426	
US	2001-286823P	P	20010426	
US	2002-289660	A2	20021106	
US	2003-693056	A2	20031024	
US	2003-693057	A2	20031024	
WO	2003-US35664	W	20031106	
US	2004-840723	A2	20040505	
US	2004-871602	A2	20040617	
US	2004-628596P	P	20041116	

OS MARPAT 139:194002

AB Combinatorial libraries of variants of discrete and defined monomer domains of proteins and immunodomains are described for use in protein engineering. Methods for generating multimers from two or more selected discrete monomer domains are also provided, along with methods for identifying multimers possessing a desired property. Presentation systems are also provided which present the discrete monomer and/or immuno-domains, selected monomer and/or immuno-domains, multimers and/or

selected multimers to allow their selection. Compns., libraries and cells
that express one or more library member, along with kits and integrated
systems, are also included in the present invention.

L4 ANSWER 3 OF 5 MEDLINE on STN DUPLICATE 1
AN 2000437199 MEDLINE
DN PubMed ID: 10821830
TI Self-assembly and supramolecular organization of EMILIN.
AU Mongiat M; Mungiguerra G; Bot S; Mucignat M T; Giacomello E; Doliana R;
Colombatti A
CS Divisione di Oncologia Sperimentale 2, Centro di Riferimento Oncologico di
Aviano, Italy.
SO The Journal of biological chemistry, (2000 Aug 18) Vol. 275, No. 33, pp.
25471-80.
Journal code: 2985121R. ISSN: 0021-9258.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
(RESEARCH SUPPORT, NON-U.S. GOV'T)
LA English
FS Priority Journals
EM 200009
ED Entered STN: 28 Sep 2000
Last Updated on STN: 28 Sep 2000
Entered Medline: 21 Sep 2000
AB The primary structure of human Elastin microfibril interface-located
protein (EMILIN), an elastic fiber-associated glycoprotein, consists of a
globular C1q domain (gC1q) at the C terminus, a short collagenous stalk, a
long region with a high potential for forming coiled-coil alpha helices,
and a cysteine-rich N-terminal sequence. It is not known whether the
EMILIN gC1q domain is involved in the assembly process and in the
supramolecular organization as shown for the similar domain of collagen X.
By employing the yeast two-hybrid system the EMILIN
gC1q domains interacted with themselves, proving for the first time that
this interaction occurs in vivo. The gC1q domain formed oligomers running
as trimers in native gels that were less stable than the comparable
trimers of the collagen X gC1q domain since they did not withstand

heating. The collagenous domain was trypsin-resistant and migrated at a size corresponding to a triple helix under native conditions. In reducing agarose gels, EMILIN also migrated as a trimer, whereas under non-reducing conditions it formed polymers of many millions of daltons. A truncated fragment lacking gC1q and collagenous domains assembled to a much lesser extent, thus deducing that the C-terminal domain(s) are essential for the formation of trimers that finally assemble into large EMILIN multimers.

L4 ANSWER 4 OF 5 MEDLINE on STN DUPLICATE 2
AN 1999429835 MEDLINE
DN PubMed ID: 10498700
TI P1 ParB domain structure includes two independent multimerization domains.
AU Surtees J A; Funnell B E
CS Department of Molecular and Medical Genetics, University of Toronto, Toronto, Ontario M5S 1A8, Canada.
SO Journal of bacteriology, (1999 Oct) Vol. 181, No. 19, pp. 5898-908.
Journal code: 2985120R. ISSN: 0021-9193.
CY United States
DT Journal; Article; (JOURNAL ARTICLE) (RESEARCH SUPPORT, NON-U.S. GOV'T)
LA English
FS Priority Journals
EM 199910
ED Entered STN: 1 Nov 1999
Last Updated on STN: 3 Mar 2000
Entered Medline: 21 Oct 1999
AB ParB is one of two P1-encoded proteins that are required for active partition of the P1 prophage in Escherichia coli. To probe the native domain structure of ParB, we performed limited proteolytic digestions of full-length ParB, as well as of several N-terminal and C-terminal deletion fragments of ParB. The C-terminal 140 amino acids of ParB form a very trypsin-resistant domain. In contrast, the N terminus is more susceptible to proteolysis, suggesting that it forms a less stably folded domain or domains. Because native ParB is a dimer in solution, we

analyzed the ability of ParB fragments to dimerize, using both the yeast two-hybrid system and in vitro chemical cross-linking of purified proteins. These studies revealed that the C-terminal 59 amino acids of ParB, a region within the protease-resistant domain, are sufficient for dimerization. Cross-linking and yeast two-hybrid experiments also revealed the presence of a second self-association domain within the N-terminal half of ParB. The cross-linking data also suggest that the C terminus is inhibitory to multimerization through the N-terminal domain in vitro. We propose that the two multimerization domains play distinct roles in partition complex formation.

L4 ANSWER 5 OF 5 CAPLUS COPYRIGHT 2007 ACS on STN
AN 1998:801698 CAPLUS
DN 130:135848
TI The β subunit of CKII interacts with the lysosomal protease cathepsin L
AU Yu, Hyun Jae; Ahn, Bong-Hyun; Bae, Young-Seuk
CS Department of Biochemistry, College of Natural Sciences, Kyungpook National University, Taegu, 702-701, S. Korea
SO Journal of Biochemistry and Molecular Biology (1998), 31(6), 611-614
CODEN: JBMBE5; ISSN: 1225-8687
PB Springer-Verlag Singapore Pte. Ltd.
DT Journal
LA English
AB Protein kinase CKII is a protein Ser/Thr kinase that is ubiquitously distributed in eukaryotic cells. Although it has been suggested that CKII plays an critical role in cell growth and proliferation, its functional significance and regulation in the cells remain poorly understood. To investigate the exact biol. function of CKII, the authors have identified proteins that interact with the subunits of CKII using the two-hybrid system. The authors have identified cathepsin L, a lysosomal protease, as a cellular protein capable of interacting with the β subunit of CKII. Cathepsin L does not interact with the α subunit of CKII, supporting the idea that the β subunit can mediate the interaction of CKII with target proteins. The authors have found that

cathepsin L has several putative CKII phosphorylation sites including Thr
84, Ser 160, Ser 270, Thr 288, and Ser 301. These data suggest that CKII
is a possible protein kinase for cathepsin L phosphorylation.
RE.CNT 20 THERE ARE 20 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

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L5 4422 (RECONSTITUTION OR COMPLEMENTATION) (4A) ACTIVITY

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L6 5 L1 AND L5

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PROCESSING COMPLETED FOR L6
L7 3 DUPLICATE REMOVE L6 (2 DUPLICATES REMOVED)

=> d l7 1-3 bib ab

L7 ANSWER 1 OF 3 MEDLINE on STN DUPLICATE 1
AN 93350342 MEDLINE
DN PubMed ID: 8347934
TI Activation and secretion of Serratia hemolysin.
AU Braun V; Ondraczek R; Hobbie S
CS Mikrobiologie II, Universitat Tubingen, Germany.
SO Zentralblatt fur Bakteriologie : international journal of medical microbiology, (1993 Apr) Vol. 278, No. 2-3, pp. 306-15. Ref: 28
Journal code: 9203851. ISSN: 0934-8840.
CY GERMANY: Germany, Federal Republic of
DT (IN VITRO)
Journal; Article; (JOURNAL ARTICLE)
(RESEARCH SUPPORT, NON-U.S. GOV'T)
General Review; (REVIEW)
LA English
FS Priority Journals
EM 199309
ED Entered STN: 1 Oct 1993
Last Updated on STN: 3 Mar 2000
Entered Medline: 16 Sep 1993
AB The hemolysin of Serratia marcescens (ShlA) is secreted into the culture
medium and forms small pores of a defined size in erythrocytes and in
black lipid membranes. The protein is synthesized as an inactive
precursor of 1608 residues which is translocated across the cytoplasmic

membrane by the Sec-export system. In the absence of the outer membrane protein ShlB, the ShlA protein (designated ShlA*) stays in the periplasm and displays about 0.1% of the activity of the secreted form. Secretion of ShlA with the help of ShlB is accompanied by its conversion to the hemolytic form. A ShlA derivative consisting of the N-terminal 238 residues of ShlA is secreted by ShlB, showing that the secretion signal resides in the amino terminal part of ShlA. ShlA* can be activated in vitro by a cell lysate containing ShlB, the activated ShlA remains hemolytic upon removal of ShlB. The assumed covalent modification of ShlA* by ShlB occurs in the N-terminus of ShlA since an amino terminal fragment (M(r) 28,000) secreted by ShlB, and a trypsin fragment of ShlA (M(r) 15,000) are both able to convert ShlA* to a hemolytic protein. In contrast to the permanent modification of ShlA* by ShlB, ShlA activity achieved by complementation with the ShlA fragments is abolished upon removal of the fragments. Apparently, the N-terminal portion of ShlA contains the information for secretion through the outer membrane and for insertion into the erythrocyte membrane. This information is lacking in ShlA* formed in the absence of ShlB but contained in the ShlA fragments formed in the presence of ShlB. The latter bind to ShlA* and direct ShlA* into the erythrocyte membrane. The fragments themselves are too short to build pores. The HpmA hemolysin of Proteus mirabilis shows extensive homology to ShlA. In vitro activation of HpmA* by ShlB and complementation by the 28 kDa ShlA fragment indicates a common activation mechanism.

L7 ANSWER 2 OF 3 EMBASE DUPLICATE 2
AN 78366209 EMBASE
DN 1978366209
TI Some effects of trypsin on the subunits of the membrane ATPase from

Escherichia coli.
AU Smith J.B.; Sternweis P.C.; Larson R.J.
CS Sect. Biochem., Molec. Cell Biol., Cornell Univ., Ithaca, N.Y. 14853,
United States
SO Progress in Clinical and Biological Research, (1978) Vol. VOL.22, pp.
545-552. .
CODEN: PCBRD2
CY United States
DT Journal
FS 004 Microbiology
029 Clinical Biochemistry
LA English
AB Five-subunit (α, β, γ, δ, ε) F1-ATPase from
E. coli (ECF1) was reconstituted by combining 2 mixtures of inactive
subunits (an αβ fraction and a γε-rich one) and
the purified δ subunit. The combination of αβ and
γε-rich fractions was sufficient for reconstituting ATPase
activity, which was achieved by dialyzing the subunits at 23° C in
the presence of Mg-ATP. Addition of the purified δ subunmit to the
reconstituted ATPase restored coupling factor activity to the enzyme. The
reconstituted enzyme was as active as the native enzyme in restoring
ATP-driven transhydrogenase activity to F1-depleted vesicles. Incubation
of the γε-rich fraction with trypsin decreased markedly the
reconstitution of ATPase activity, whereas treatment of
the αβ fraction with trypsin under the same conditions had no
significant effect. ECF1 containing only the α and β subunits,
which was prepared by trypsin digestion, was highly active hydrolytically
but remained inactive as a coupling factor even after the addition of the
γε-rich fraction and δ. The inhibition of ECF1 by the
purified ε subunit was reversed by trypsin.
Thus, while trypsin inactivates the γ and ε subunits of
ECF1, the α and/or β subunits are altered in a way which only
inactivates the coupling factor activity of the enzyme without affecting
its ATPase activity or the reconstitution of ATPase
activity after cold inactivation. Since exposure of the α
and β subunits to trypsin does not appear to alter their interaction
with added γ and ε, it may be that the loss of coupling
factor activity is due to a modification in α or β which
disrupts their interaction with the membrane attachment subunit (δ).

L7 ANSWER 3 OF 3 BIOSIS COPYRIGHT (c) 2007 The Thomson Corporation on STN
AN 1979:141571 BIOSIS
DN PREV197967021571; BA67:21571
TI THE FOLDING OF PANCREATIC ELASTASE INDEPENDENT DOMAIN RE FOLDING AND INTER DOMAIN INTERACTION.
AU GHELIS C [Reprint author]; TEMPETE-GAILLOURDET M; YON J M
CS LAB ENZYMOL PHYS-CHIM MOL, UNIV PARIS-SUD, 91405, ORSAY, FR
SO Biochemical and Biophysical Research Communications, (1978) Vol. 84, No. 1, pp. 31-36.
CODEN: BBRCA9. ISSN: 0006-291X.
DT Article
FS BA
LA ENGLISH
AB The role of domains in the refolding of [pig pancreatic] elastase, a 2 domain protein, was investigated. Fragment 126-245, corresponding to 1 of the 2 domains, is able to refold independently. The in vitro complementation of the 2 domains lead to a molecule having the overall conformation of the native protein and only a weak but significant activity.

=> s l4 and l7
L8 0 L4 AND L7

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NEWS 5 DEC 18 MARPAT to CA/CAplus accession number crossover limit increased
to 50,000
NEWS 6 DEC 18 MEDLINE updated in preparation for 2007 reload
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NEWS 18 FEB 23 KOREAPAT enhanced with IPC 8 features and functionality
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to 300,000 in multiple databases
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NEWS 28 MAR 30 RDISCLOSURE reloaded with enhancements
NEWS 29 MAR 30 INPADOCDB will replace INPADOC on STN
NEWS 30 APR 02 JICST-EPLUS removed from database clusters and STN

NEWS EXPRESS NOVEMBER 10 CURRENT WINDOWS VERSION IS V8.01c, CURRENT MACINTOSH VERSION IS V6.0c(ENG) AND V6.0Jc(JP), AND CURRENT DISCOVER FILE IS DATED 25 SEPTEMBER 2006.

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FULL ESTIMATED COST	0.21	0.21

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FILE 'EMBASE' ENTERED AT 09:56:27 ON 05 APR 2007

FILE 'BIOSIS' ENTERED AT 09:56:27 ON 05 APR 2007

FILE 'CAPLUS' ENTERED AT 09:56:27 ON 05 APR 2007

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=> s (protease or peptidase or proteinase) (4A) (domain or fragment
or subunit or region eptitope or motif)
L1       11554 (PROTEASE OR PEPTIDASE OR PROTEINASE) (4A) (DOMAIN OR
FRAGMENT
               OR SUBUNIT OR REGION EPTITOPE OR MOTIF)

=> s reconstitution (4A) activity
L2        3341 RECONSTITUTION (4A) ACTIVITY

=> s l1 (10A) l2
L3           0 L1 (10A) L2

=> s l1 and l2
L4           3 L1 AND L2

=> duplicate
ENTER REMOVE, IDENTIFY, ONLY, OR (?):remove
ENTER L# LIST OR (END):l4
DUPLICATE PREFERENCE IS 'MEDLINE, BIOSIS, CAPLUS'
KEEP DUPLICATES FROM MORE THAN ONE FILE?  Y/(N):n
PROCESSING COMPLETED FOR L4
L5           1 DUPLICATE REMOVE L4 (2 DUPLICATES REMOVED)

=> d l5 1 bib ab

L5   ANSWER 1 OF 1     MEDLINE on STN                    DUPLICATE 1
AN   89214013     MEDLINE
DN   PubMed ID: 2854124
TI   Carboxyl-terminal truncation and site-directed mutagenesis of
the EF hand
     structure-domain of the small subunit of rabbit
     calcium-dependent protease.
AU   Minami Y; Emori Y; Imajoh-Ohmi S; Kawasaki H; Suzuki K
CS   Department of Molecular Biology, Tokyo Metropolitan Institute of
Medical
     Science.
SO   Journal of biochemistry, (1988 Dec) Vol. 104, No. 6, pp. 927-33.

     Journal code: 0376600. ISSN: 0021-924X.
CY   Japan
DT   Journal; Article; (JOURNAL ARTICLE)
     (RESEARCH SUPPORT, NON-U.S. GOV'T)
LA   English
FS   Priority Journals
EM   198905
ED   Entered STN: 6 Mar 1990
     Last Updated on STN: 6 Mar 1990
     Entered Medline: 26 May 1989
AB   A mutant of the small subunit of rabbit calcium-dependent
     protease lacking the amino-terminal one-fourth produced in
```

Escherichia coli could associate with the native large subunit to exert protease activity. Deletion of a few carboxyl-terminal residues of this variant small subunit caused a significant decrease in the protease activity after reconstitution with the native large subunit. Loss of the fourth EF hand loop region by further truncation of the variant small subunit made interaction with the large subunit impossible. The calcium binding assay revealed that the fourth EF hand structure of the rabbit small subunit, which has been previously demonstrated to possess two calcium-binding sites, can bind calcium ions. Furthermore it was established by site-directed mutagenesis that the first EF hand structure, in addition to the fourth one, is capable of binding calcium ions. Replacement of amino acids in the EF hand structure affected interaction with the native large subunit or the calcium sensitivity of the reconstituted product. These findings indicate that the EF hand structure-domain of the small subunit is essential for the full protease activity.

```
=> s complementation (4A) activity
L6         1091 COMPLEMENTATION (4A) ACTIVITY

=> s l1 (10A) l6
L7            0 L1 (10A) L6

=> s l1 and l6
L8            8 L1 AND L6

=> duplicate
ENTER REMOVE, IDENTIFY, ONLY, OR (?):remove
ENTER L# LIST OR (END):l8
DUPLICATE PREFERENCE IS 'MEDLINE, EMBASE, BIOSIS, CAPLUS'
KEEP DUPLICATES FROM MORE THAN ONE FILE?  Y/(N):n
PROCESSING COMPLETED FOR L8
L9             3 DUPLICATE REMOVE L8 (5 DUPLICATES REMOVED)

=> d l9 1-3 bib ab

L9   ANSWER 1 OF 3     MEDLINE on STN                    DUPLICATE 1
AN   2007002178     MEDLINE
DN   PubMed ID: 17101804
TI   Variable and tissue-specific subunit composition of
mitochondrial m-AAA
     protease complexes linked to hereditary spastic paraplegia.
AU   Koppen Mirko; Metodiev Metodi D; Casari Giorgio; Rugarli Elena
I; Langer
     Thomas
CS   Institut fur Genetik, Universitat zu Koln, Zulpicher Strasse,
0674 Koln,
     Germany.
SO   Molecular and cellular biology, (2007 Jan) Vol. 27, No. 2, pp.
758-67.
     Electronic Publication: 2006-11-13.
     Journal code: 8109087. ISSN: 0270-7306.
CY   United States
DT   Journal; Article; (JOURNAL ARTICLE)
     (RESEARCH SUPPORT, NON-U.S. GOV'T)
LA   English
FS   Priority Journals
EM   200702
ED   Entered STN: 4 Jan 2007
     Last Updated on STN: 6 Feb 2007
     Entered Medline: 5 Feb 2007
AB   The m-AAA protease, an ATP-dependent proteolytic complex in the
     mitochondrial inner membrane, controls protein quality and
regulates
     ribosome assembly, thus exerting essential housekeeping
functions within
     mitochondria.  Mutations in the m-AAA protease subunit
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paraplegin cause axonal degeneration in hereditary spastic paraplegia (HSP), but the basis for the unexpected tissue specificity is not understood. Paraplegin assembles with homologous Afg3l2 subunits into hetero-oligomeric complexes which can substitute for yeast m-AAA proteases, demonstrating functional conservation. The function of a third paralogue, Afg3l1 expressed in mouse, is unknown. Here, we analyze the assembly of paraplegin into m-AAA complexes and monitor consequences of paraplegin deficiency in HSP fibroblasts and in a mouse model for HSP.

Our findings reveal variability in the assembly of m-AAA proteases in mitochondria in different tissues. Homo-oligomeric Afg3l1 and Afg3l2 complexes and hetero-oligomeric assemblies of both proteins with paraplegin can be formed. Yeast complementation studies demonstrate the proteolytic activity of these assemblies.

Paraplegin deficiency in HSP does not result in the loss of m-AAA protease activity in brain mitochondria. Rather, homo-oligomeric Afg3l2 complexes accumulate, and these complexes can substitute for housekeeping functions of paraplegin-containing m-AAA complexes. We therefore propose that the formation of m-AAA proteases with altered substrate specificities leads to axonal degeneration in HSP.

L9 ANSWER 2 OF 3 MEDLINE on STN DUPLICATE 2
AN 1999126015 MEDLINE
DN PubMed ID: 9928935
TI The protease activity of a calpain-like cysteine protease in Saccharomyces cerevisiae is required for alkaline adaptation and sporulation.
AU Futai E; Maeda T; Sorimachi H; Kitamoto K; Ishiura S; Suzuki K
CS Department of Molecular Biology, Institute of Molecular and Cellular Biosciences, University of Tokyo, Japan.
SO Molecular & general genetics : MGG, (1999 Jan) Vol. 260, No. 6, pp. 559-68.
Journal code: 0125036. ISSN: 0026-8925.
CY GERMANY: Germany, Federal Republic of
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals

EM 199902
ED Entered STN: 1 Mar 1999
Last Updated on STN: 3 Mar 2000
Entered Medline: 18 Feb 1999
AB Abstract Saccharomyces cerevisiae has only one putative gene (designated
CPL1) for a cysteine protease with a protease
domain similar to that of calpain. This gene product shows
significant sequence similarity to PalBp, a fungal (Emericella nidulans)
calpain-like protease that is responsible for adaptation under alkaline
conditions, both in the protease domain and the
domain following the protease domain. CPL1
disruptant strains show impaired growth at alkaline pH, but no obvious
growth defects under acidic pH conditions. This phenotype is complemented
by the wild-type CPL1 gene, and its protease activity is
essential for complementation. Disruption of CPL1 also causes
reduced sporulation efficiency and promotes the degradation of the
transcription factor Rim101p, which is involved in the sporulation pathway
and has been shown to accumulate in a C-terminally truncated, active form
under alkaline conditions. Furthermore, expression of the C-terminally
truncated Rim101p suppressed the alkaline sensitivity associated with CPL1
disruption. These results indicate that a calpain-like cysteine protease,
Cpl1p, plays an important role in alkaline adaptation and sporulation
processes, via regulation of the turnover and processing of the
transcription factor Rim101p.

L9 ANSWER 3 OF 3 CAPLUS COPYRIGHT 2007 ACS on STN
AN 1999:112529 CAPLUS
DN 130:308897
TI The protease activity of a calpain-like cysteine protease in Saccharomyces
cerevisiae is required for alkaline adaptation and sporulation
AU Futai, E.; Maeda, T.; Sorimachi, H.; Kitamoto, K.; Ishiura, S.; Suzuki, K.
CS Laboratory of Molecular Structure and Function Department of Molecular
Biology Institute of Molecular and Cellular Biosciences, University of
Tokyo, Tokyo, 113-0032, Japan
SO Molecular and General Genetics (1998), 260(6), 559-568

CODEN: MGGEAE; ISSN: 0026-8925
PB Springer-Verlag
DT Journal
LA English
AB Saccharomyces cerevisiae has only one putative gene (designated CPL1) for a cysteine protease with a protease domain similar to that of calpain. This gene product shows significant sequence similarity to PalBp, a fungal (Emericella nidulans) calpain-like protease that is responsible for adaptation under alkaline conditions, both in the protease domain and the domain following the protease domain. CPL1 disruptant strains show impaired growth at alkaline pH, but no obvious growth defects under acidic pH conditions. This phenotype is complemented by the wild-type CPL1 gene, and its protease activity is essential for complementation. Disruption of CPL1 also causes reduced sporulation efficiency and promotes the degradation of the transcription factor Rim101p, which is involved in the sporulation pathway and has been shown to accumulate in a C-terminally truncated, active form under alkaline conditions. Furthermore, expression of the C-terminally truncated Rim101p suppressed the alkaline sensitivity associated with CPL1 disruption. These results indicate that a calpain-like cysteine protease, Cpl1p, plays an important role in alkaline adaptation and sporulation processes, via regulation of the turnover and processing of the transcription factor Rim101p.
RE.CNT 29 THERE ARE 29 CITED REFERENCES AVAILABLE FOR THIS RECORD
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Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L3	2651401	s (chymotrypsin or trypsin or elastase or cathepsin or granzyme or chymase or tryptase) near4 (domain or fragment or subunit or region or epitope or motif)	US-PGPUB; USPAT	OR	OFF	2007/04/05 11:23
L4	2523	(chymotrypsin or trypsin or elastase or cathepsin or granzyme or chymase or tryptase) near4 (domain or fragment or subunit or region or epitope or motif)	US-PGPUB; USPAT	OR	OFF	2007/04/05 11:26
L5	3426	(reconstitution or complementation) near4 activity	US-PGPUB; USPAT	OR	OFF	2007/04/05 11:24
L6	0	l4 near10 l5	US-PGPUB; USPAT	OR	OFF	2007/04/05 11:24
L7	123	l4 and l5	US-PGPUB; USPAT	OR	OFF	2007/04/05 11:24
L8	0	l4 same 5	US-PGPUB; USPAT	OR	OFF	2007/04/05 11:25
L9	0	l4 near30 l5	US-PGPUB; USPAT	OR	OFF	2007/04/05 11:25
L10	117	l7 and (two adj hybrid)	US-PGPUB; USPAT	OR	OFF	2007/04/05 11:25
L11	153	(chymotrypsin or trypsin or elastase or cathepsin or granzyme or chymase or tryptase) near4 (fusion adj protein)	US-PGPUB; USPAT	OR	OFF	2007/04/05 11:26
L12	0	l10 and l11	US-PGPUB; USPAT	OR	OFF	2007/04/05 11:26

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with preparation role
NEWS 4 DEC 18 CA/CAplus patent kind codes updated
NEWS 5 DEC 18 MARPAT to CA/CAplus accession number crossover limit increased
to 50,000
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NEWS 7 DEC 27 CA/CAplus enhanced with more pre-1907 records
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multiple databases
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NEWS 17 FEB 15 RUSSIAPAT enhanced with pre-1994 records
NEWS 18 FEB 23 KOREAPAT enhanced with IPC 8 features and functionality
NEWS 19 FEB 26 MEDLINE reloaded with enhancements
NEWS 20 FEB 26 EMBASE enhanced with Clinical Trial Number field
NEWS 21 FEB 26 TOXCENTER enhanced with reloaded MEDLINE
NEWS 22 FEB 26 IFICDB/IFIPAT/IFIUDB reloaded with enhancements
NEWS 23 FEB 26 CAS Registry Number crossover limit increased from 10,000

to 300,000 in multiple databases
NEWS 24 MAR 15 WPIDS/WPIX enhanced with new FRAGHITSTR display format
NEWS 25 MAR 16 CASREACT coverage extended
NEWS 26 MAR 20 MARPAT now updated daily
NEWS 27 MAR 22 LWPI reloaded
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FILE 'BIOSIS' ENTERED AT 18:47:25 ON 12 APR 2007

FILE 'CAPLUS' ENTERED AT 18:47:25 ON 12 APR 2007

```
=> S (picornavirus or potyvirus or rhinovirus or enterovirus or
echovirus or (coxsackie virus) or (hepatitis virus) or cardiovirus)
(4A) (cysteine protease)
L1          22 (PICORNAVIRUS OR POTYVIRUS OR RHINOVIRUS OR
ENTEROVIRUS OR ECHOV
               IRUS OR (COXSACKIE VIRUS) OR (HEPATITIS VIRUS) OR
CARDIOVIRUS)
              (4A) (CYSTEINE PROTEASE)

=> S L1 (8A) (reconstitution or (two-hybrid) or (2-hybrid) or
complementation)
L2           0 L1 (8A) (RECONSTITUTION OR (TWO-HYBRID) OR (2-HYBRID)
OR COMPLEM
               ENTATION)

=> s l1 (8A) (domain or fragment)
L3           0 L1 (8A) (DOMAIN OR FRAGMENT)

=> s l1 (8A) structure
L4           0 L1 (8A) STRUCTURE

=> duplicate
ENTER REMOVE, IDENTIFY, ONLY, OR (?):remove
ENTER L# LIST OR (END):l1
DUPLICATE PREFERENCE IS 'MEDLINE, EMBASE, BIOSIS, CAPLUS'
KEEP DUPLICATES FROM MORE THAN ONE FILE?  Y/(N):n
PROCESSING COMPLETED FOR L1
L5           12 DUPLICATE REMOVE L1 (10 DUPLICATES REMOVED)

=> s (3C cysteine protease)
L6          16 (3C CYSTEINE PROTEASE)

=> S L6 (8A) (reconstitution or (two-hybrid) or (2-hybrid) or
complementation)
L7           0 L6 (8A) (RECONSTITUTION OR (TWO-HYBRID) OR (2-HYBRID)
OR COMPLE
               MENTATION)

=> s (trypsin or chymotrypsin)(8A) (reconstitution or (two-hybrid) or
(2-hybrid) or complementation)
L8         117 (TRYPSIN OR CHYMOTRYPSIN)(8A) (RECONSTITUTION OR
(TWO-HYBRID)
               OR (2-HYBRID) OR COMPLEMENTATION)

=> s (trypsin or chymotrypsin) (4A) (domain or fragment or fusion
protein)
L9        3014 (TRYPSIN OR CHYMOTRYPSIN) (4A) (DOMAIN OR FRAGMENT OR
FUSION
               PROTEIN)
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=> s l8 and l9
L10           5 L8 AND L9

=> duplicate
ENTER REMOVE, IDENTIFY, ONLY, OR (?):remove
ENTER L# LIST OR (END):l10
DUPLICATE PREFERENCE IS 'MEDLINE, EMBASE, BIOSIS, CAPLUS'
KEEP DUPLICATES FROM MORE THAN ONE FILE?  Y/(N):no
PROCESSING COMPLETED FOR L10
L11            2 DUPLICATE REMOVE L10 (3 DUPLICATES REMOVED)

=> d l11 1-2 bib ab

L11  ANSWER 1 OF 2     MEDLINE on STN                    DUPLICATE 1
AN   1998035059     MEDLINE
DN   PubMed ID: 9367764
TI   Complementation of peptide fragments of the single
     domain protein chymotrypsin inhibitor 2.
AU   Ladurner A G; Itzhaki L S; de Prat Gay G; Fersht A R
CS   MRC Cambridge Centre for Protein Engineering, MRC Centre, UK.
SO   Journal of molecular biology, (1997 Oct 17) Vol. 273, No. 1, pp.
317-29.
     Journal code: 2985088R. ISSN: 0022-2836.
CY   ENGLAND: United Kingdom
DT   Journal; Article; (JOURNAL ARTICLE)
     (RESEARCH SUPPORT, NON-U.S. GOV'T)
LA   English
FS   Priority Journals
EM   199712
ED   Entered STN: 9 Jan 1998
     Last Updated on STN: 9 Jan 1998
     Entered Medline: 5 Dec 1997
AB   Chymotrypsin inhibitor 2 (CI2) folds kinetically as a single
domain
     protein.  It has been shown that elements of native secondary
structure do
     not significantly form in fragments as the 64 residue protein is
     progressively increased in length from its N terminus, until at
least 60
     residues are present.  Here, we analyse peptides of increasing
length from
     the C terminus and find that native-like structure is not
present even in
     the largest, fragment (7-64).  We have examined sets of peptides
of the
     form (1 - x) and ((x + 1)-64) to detect complementation.  The
only pair
     that readily complements and gives native-like structure is
(1-40) and
     (41-64), where cleavage occurs in the protease-binding loop of
CI2.  But,
```

all the pairs of peptides (1 - x) + (41-64) complement for x > 40, as do all pairs of (1-40) + (x-64), where x < 40. The resultant complexes appear to be equivalent to (1-40). (41-64) with the overlapping sequence being unstructured. Thus, the folding of CI2 is extremely co-operative, and interactions have to be made between subdomains (1-40) and (41-64). This is consistent with the mechanism proposed for the folding pathway of intact CI2 in which a diffuse nucleus is formed in the transition state between the alpha-helix in the N-terminal region of the protein and conserved hydrophobic contacts in the C-terminal region of the polypeptide. It is with these protein design features that CI2 can be an effective protease inhibitor.

L11 ANSWER 2 OF 2 CAPLUS COPYRIGHT 2007 ACS on STN
AN 1994:429728 CAPLUS
DN 121:29728
TI Generation of a Family of Protein Fragments for Structure-Folding Studies.
1. Folding Complementation of Two Fragments of Chymotrypsin Inhibitor-2 Formed by Cleavage at Its Unique Methionine Residue
AU Prat Gay, G. de; Fersht, Alan R.
CS Department of Chemistry, Cambridge University, Cambridge, CB2 1EW, UK
SO Biochemistry (1994), 33(25), 7957-63
CODEN: BICHAW; ISSN: 0006-2960
DT Journal
LA English
AB The suitability of the barley chymotrypsin inhibitor-2 for study by fragmentation and complementation has been analyzed. The primary residue for binding to proteases, Met-59 (the unique methionine in the sequence), lies in a broad, solvent-exposed loop. The bond between Met-59 and Glu-60 was cleaved by cyanogen bromide. The two fragments thus obtained, i.e., CI-2(20-59) and CI-2(60-83), associate (KD = 42 nM) to yield a complex that has fluorescence and CD spectra identical to those of uncleaved chymotrypsin inhibitor-2. Recovery of native-like structure is further indicated by the ability of the complex to inhibit chymotrypsin,

although the [I]50% is 140-fold higher than for the uncleaved inhibitor.

CI-2(60-83) appears to be highly disordered in water, but fragment

CI(20-59) forms a significant structure, as judged by its circular

dichroism spectra and evidence from one-dimensional NMR. The CD spectra

of CI-2(20-59) approach the baseline in 4 M guanidinium chloride but

display characteristics of an α-helix in the presence of

trifluoroethanol. Anal. ultracentrifugation shows no concentration-dependent

change in the mol. weight of the monomer of CI-2(20-59). Both one- and

two-dimensional NMR of the complex [CI-2(20-59)·(60-83)] show

unequivocally the presence of a folded structure, which appears to be

slightly different from the uncleaved native protein.